Application No.: 10/706791 Customer No. 25291

Inventors: Christopher William Aston et al.
Attorney Docket No.: AM101119
Title: METHODS AND COMPOSITIONS FOR TREATING....

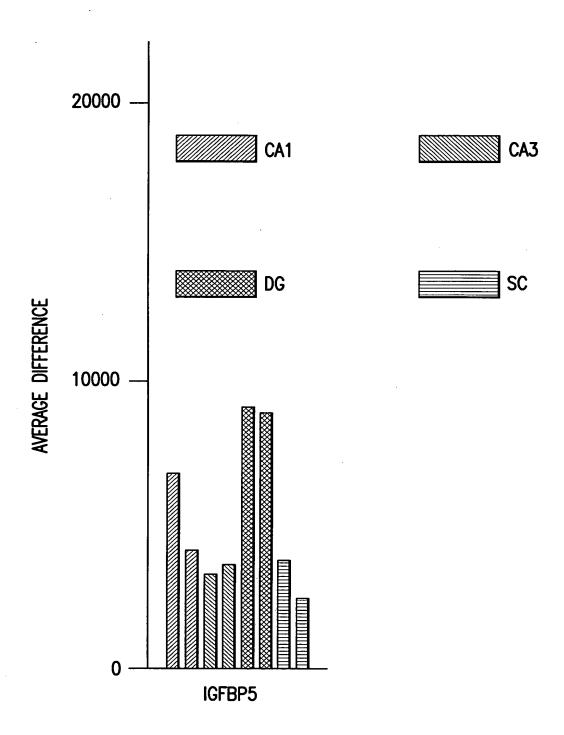
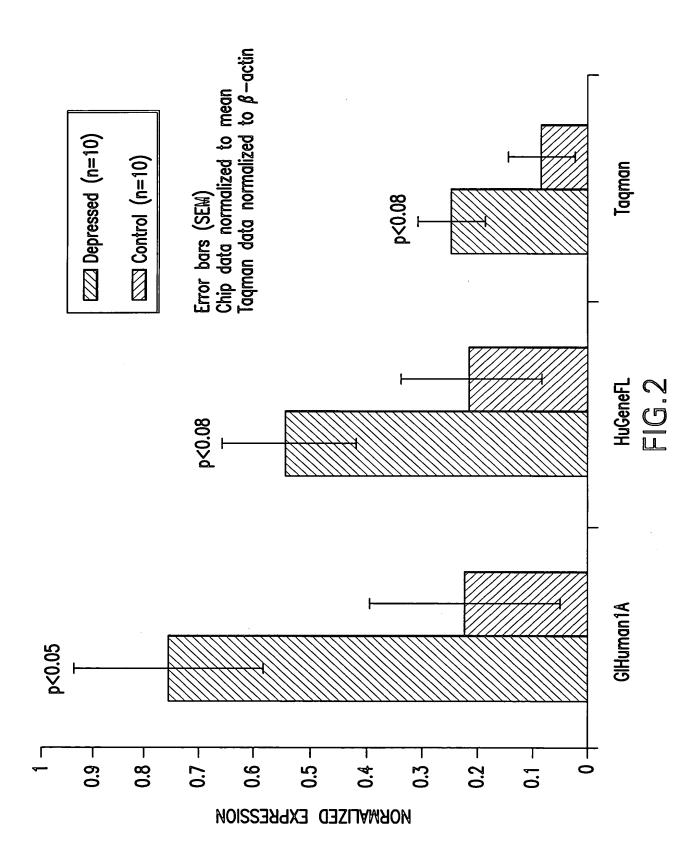


FIG.1

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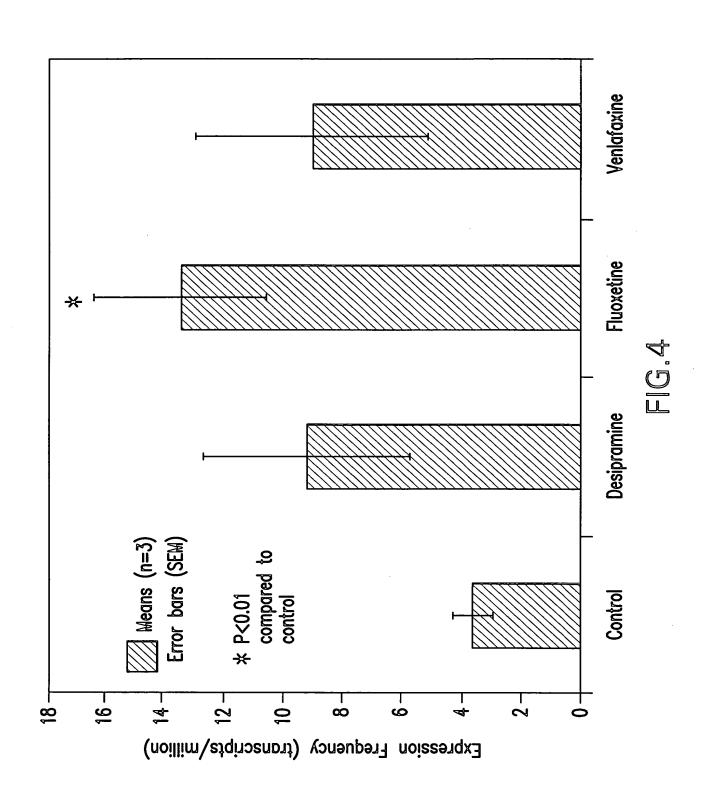
Application No.: 10/706791 Customer Inventors: Christopher William Aston et al. Customer No. 25291 Attorney Docket No.: AM101119 Title: METHODS AND COMPOSITIONS FOR TREATING .... 140 140 Affy Name: 40422\_at Cluster Name: insulin—like growth factor binding protein 2(36kD) 127 152 125 110 011 106 Expression frequency (transcripts/million) 96 96 08 08 9 67 92 20 90 32 32 50 50 ς ς 01-01 52. -52 -33 04-04 9 28/ Depressed (n=12) Control (n=14) Normal Sample set ALL Depressed Sample set ALL 1.3 Fold change p<0.2 MARGINAL MARGINAL **PRESENT** ABSENT ABSENT

FIG.3

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Species	Rat
Mr/pl	17079/ 9.5
Protein Area Coverage	28%
MOWSE	P08025 7.07E+01
Venlafaxine Fluoxetine Accession# MOWSE Protein Mr/pl Species (Fold change) change)	P08025
Fluoxetine (Fold change)	2.5
Venlafaxine (Fold change)	2.9
Function	IGF-1 A GH is an important precursor regulator of IGF-1 expression. Secreted/Growth- promoting activity.
Protein Identity	IGF-1 A precursor
Original Protein gel spot # Identity	87

Fold Change Following Treatment

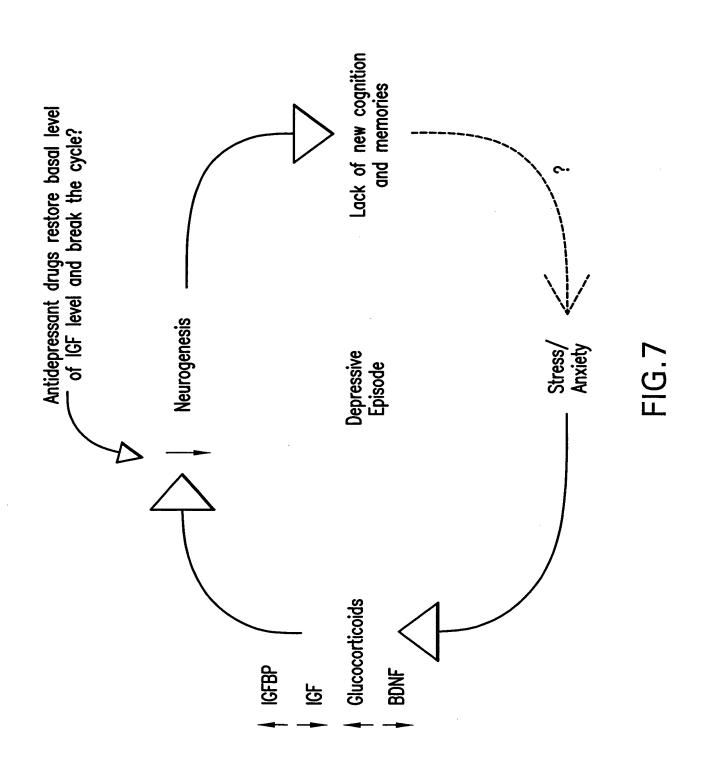
Application No.: 10/706791

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Customer No. 25291

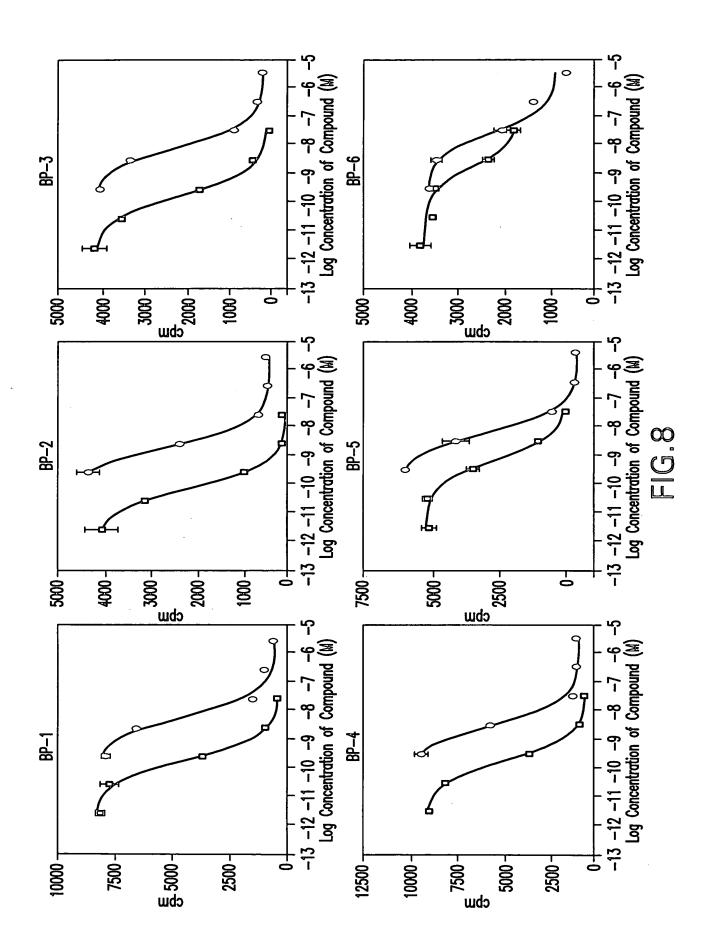
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1MORAR PTLWAAALTL LVLLRGPPVA RAGASSGGLG PVVRCEPCDA MLPVVGCPAL PLPPPPLLPL LPLLLLLLGA SGGGGARAE VLFRCPPCTP	100	150 DE ARPLQALLDG RGLCVNASAV SRLRAYLLPA DE EKPLHALLHG RGVCLNEKSY SS ELPLQALVMG EGTCEKRRDA EYGASPE SV EKPLHTLMHG QGVCMELA EIEAIQE SE QQPLHALTRG QGACVQESDA SAPHAAEAGS DD EAPLRALLLG RGRCLPAR
IGFBP3_proteMORAR PTLWAAALTL IGFBP5_prote	IGFBP3_prote RALAQCAPPP IGFBP5_prote KALSMCPPSP IGFBP4_prote ERLAACGPPP VAPPAAVAAV IGFBP4_prote EKLARCRPP. IGFBP1_prote EKLALCPP. IGFBP6_prote GVQAGCPGGCVEEED IGFBP7_prote	IGFBP3_prote CGIYTERCGS GLRCQPSPDE IGFBP5_prote CGVYTPRCGQ GLRCYPHPGS IGFBP4_prote CGVYTPRCGS GLRCYPPRGV IGFBP1_prote CGVYTPNCAP GLGCKPPKDD IGFBP7_prote

200 HSKIIIIKKG HTRISELKAE MKELAVF KHFAKI ISTYDGSKAL	250	PCRREMEDTL PCRRHMEASL PCQQELDQVL SCQSELHRAL PCRIELYRVV PCRRHLDSVL	300 KGRKRGFCWC LNGQRGECWC LDGQRGKCWC MDGEAGLCWC QGQRRGPCWC
SPSVSS.THR VSDPK.FKPL EPTTSEMAEE TYSPKIFRPK STMNMLGGGG SAGRKPLKSG HPNNSFSPCS AHDRRCLQLMAPS EEDHSILWDA NPKESKPQAG TA		NFS SESKRETEYG NTAHPRIISA PEMRQESEQG GKHHLGLEEP KKLRPPPART GKMKVNGAPR EDARPVP.QGE GTSTTPSQPN SAGVQPTEMG	300 VHIPNCDKKG FYKKKQCRPS KGRKRGFCWC VYLPNCDRKG FYKRKQCKPS RGRKRGICWC LHIPNCDKHG LYNLKQCKMS LNGQRGECWC IPIPNCDRNG NFHPKQCHPA LDGQRGKCWC FYLPNCNKNG FYHSRQCETS MDGEAGLCWC LVVPNCDHRG FYRKRQCRSS QGQRRGPCWC
EEDRSAGSVE SPSVSS.THR KIERDSREHE EPTTSEMAEE EGGLVENHVD STMNMLGGGG EGD HPNNSFSPCS EEELLDNFHLMAPSE NPKESKPQAG		DYSEQSTDTQ NFS SESKRETEYG TQSKFVGGAE NTAHPRIISA PEMRQESEQG TEQHRQMGKG GKHHLGLEEP KKLRPPPART TSG GKMKVNGAPR EDARPVP.QGE	VHIPNCDKKG VYLPNCDRKG LHIPNCDKHG IPIPNCDRNG FYLPNCNKNG LVVPNCDHRG
EEDRSAGSVE KIERDSREHE EGGLVENHVD EGD EEELLDNFH.		DYSEQSTDTQ TQSKFVGGAE TEQHRQMGKG TSG VNRRDQQRNP	PRA PRA ERGPLEHLYS QSRTHEDLYF QETSGEEISK QTEVYRGAQT
151 PPAPGNASESREQV QVADMGDDHS SLQPSDKD PESPESTEITAPAVAE	201	AVKKDRRKKL AVKKDRRKKLREKVRPRS HVTNIKKWK.	251 NHLKFLNVLS PRA GELKASPRMV PRA ERISTMRLPD ERGPLEHLYS ERLAAS QSRTHEDLYF ESLAKA QETSGEEISK QQL QTEVYRGAQT
IGFBP3_prote IGFBP5_prote IGFBP4_prote IGFBP1_prote IGFBP6_prote IGFBP6_prote		IGFBP3_prote HAKDSQRYKV IGFBP5_prote AVKKDRRKKL IGFBP4_proteREKV IGFBP1_prote HVTNIKKWK. IGFBP6_proteRPQD IGFBP7_prote	IGFBP3_prote IGFBP5_prote IGFBP2_prote IGFBP4_prote IGFBP1_prote IGFBP6_prote IGFBP7_prote

350	***************************************	-	1 0				M ERPSLRALLL
	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	E	EARGVHTORM	Entrument			4
	HCYSMQSK~~	QCHTFDSSNV	<b>ECHLFYNEQQ</b>	DCHQLADSFR	NCQIYFNVQN	SCPTGSSG~~	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
1	QYTTKGKEDV	GMEYV. DGDF	GAPTI.RGDP	GGLEP.KGEL	GSPEI.RGDP	GSPD. GNGSS	
301	VD.KYGQPLP	VD.KYGMKLP	VNPNTGKLIQ	VDRKTGVKLP	VYPWNGKRIP	VD.RMGKSLP	
	IGFBP3_prote VD. KYGQPUP QYTTKGKEDV HCYSMQSK~~	IGFBP5_prote VD.KYGMKLP GMEYV.DGDF QCHTFDSSNV E	IGFBP2_prote VNPNTGKLIQ GAPTI.RGDP ECHLFYNEQQ EARGVHTORM Q	IGFBP4_prote VDRKTGVKUP GQLEP.KGEL DCHQLADSFR E	IGFBP1_prote VYPWNGKRIP GSPEI.RGDP NCQIYFNVQN	IGFBP6_prote VD.RMGKSLP GSPD.GNGSS SCPTGSSG~~	IGFBP7_prote hadrandambarran recover

FIG. 90

